RAW SEQUENCE LISTING ERROR REPORT
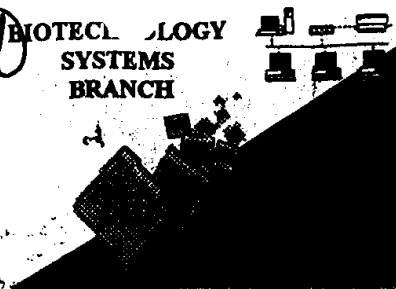
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable ~~...~~

Application Serial Number: 09/869,004

Source: Pct/09

Date Processed by STIC: 7/9/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER: INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT WITH A NOTICE TO COMPLY; or CALLING THE APPLICANT AND FAXING A COPY OF THIS PRINTOUT. WITH A NOTICE TO COMPLY. FOR COMMENTS OR QUESTIONS, PLEASE CONTACT MARK SPENCER 703-308-1212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable Form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/869,004_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino Numbering — The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length — Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence

(2) INFORMATION FOR SEQ ID NO X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO.X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence

<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.

11_____Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)

12 ✓_____PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

RAW SEQUENCE LISTING   DATE: 07/09/2001
PATENT APPLICATION: US/09/869,004   TIME: 10:11:50

Input Set : A:\Ru-0076.app
Output Set: N:\CRF3\07092001\I869004.raw

C--> 3 <140> CURRENT APPLICATION NUMBER: US/09/869,004   *see next page*
C--> 3 <141> CURRENT FILING DATE: 2001-06-22   Does Not Comply
W--> 0 <110> APPLICANT: Corrected Diskette Needed
W--> 0 <120> TITLE INVENTION:
W--> 0 <130> FILE REFERENCE:
     3 <150> PRIOR APPLICATION NUMBER: 60/113,731
     4 <151> PRIOR FILING DATE: 1998-12-23
     6 <160> NUMBER OF SEQ ID NOS: 3
     8 <170> SOFTWARE: PatentIn Ver. 2.0
    10 <210> SEQ ID NO: 1
    11 <211> LENGTH: 13
    12 <212> TYPE: DNA
    13 <213> ORGANISM: Artificial Sequence
    15 <220> FEATURE:
    16 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
    18 <400> SEQUENCE: 1
    19 gcgtacacat gcg   13
    21 <210> SEQ ID NO: 2
    22 <211> LENGTH: 13
    23 <212> TYPE: DNA
    24 <213> ORGANISM: Artificial Sequence
    26 <220> FEATURE:
    27 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
    29 <400> SEQUENCE: 2
    30 gcgatgtgta cgc   13
    32 <210> SEQ ID NO: 3
    33 <211> LENGTH: 13
    34 <212> TYPE: DNA
    37 <213> ORGANISM: Artificial Sequence
    39 <220> FEATURE:
    3F <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic *Delete*
    39   n=basi: furan
    41 <220> FEATURE:
    42 <221> NAME/KEY: misc_feature
    13 <222> LOCATION: (7)   *X 2237*   *Explanation for "n" or "Xaa" goes*
    45 <400> SEQUENCE: 3   *on its own*
W--> 46 cgcatgngta cgc   13   *<2237 line.*

*FYI: "n" can only represent
a single nucleotide
(base)
nothing else*

VERIFICATION SUMMARY   DATE: 07/09/2001
PATENT APPLICATION: **US/09/869,004**   TIME: 10:11:51

Input Set : **A:\Ru-0076.app**
Output Set: **N:\CRF3\07092001\I869004.raw**

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L:3 M:270 C: Current Application Number differs, Replaced Current Application No
L:3 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, APPLICANT NAME
L:0 M:201 W: Mandatory field data missing, TITLE INVENTION
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
```